



SEQUENCE LISTING

<110> Denney, Jr., Dan W.
<120> Vaccines for Treatment of Lymphoma and Leukemia
<130> GENITOPE-03849
<140> 09/370,453
<141> 1999-08-09
<160> 77
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gac	act	ggg	aaa	aca	atg	caa	act	ttg	ctt	tcc	ctg	gtt	aag	cag	tac								546											
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Arg Ser Val Gly Tyr Arg Pro Asp Phe Val Gly Phe Glu Ile Pro Asp
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Tyr Ile Lys Ala Leu Asn Arg Asn Ser Asp Arg Ser Ile Pro Met Thr
 85 90 95

Val Asp Phe Ile Arg Leu Lys Ser Tyr Cys Asn Asp Gln Ser Thr Gly
 100 105 110

Asp Ile Lys Val Ile Gly Gly Asp Asp Leu Ser Thr Leu Thr Gly Lys
 115 120 125

Asn Val Leu Ile Val Glu Asp Ile Ile Asp Thr Gly Lys Thr Met Gln
 130 135 140

Thr Leu Leu Ser Leu Val Lys Gln Tyr Ser Pro Lys Met Val Lys Val
 145 150 155 160

Ala Ser Leu Leu Val Lys Arg Thr Ser Arg Ser Val Gly Tyr Arg Pro
 165 170 175

Asp Phe Val Gly Phe Glu Ile Pro Asp Lys Phe Val Val Gly Tyr Ala
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<222> (13)..(573)

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Asn Met Gly Ile Gly Lys Asn Gly Asp Leu Pro Trp Pro Pro Leu Arg
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aac gag ttc aag tac ttc caa aga atg acc aca acc tct tca gtg gaa 147
Asn Glu Phe Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu
30              35              40              45

ggt aaa cag aat ctg gtg att atg ggt agg aaa acc tgg ttc tcc att 195
Gly Lys Gln Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile
50              55              60

cct gag aag aat cga cct tta aag gac aga att aat ata gtt ctc agt 243
Pro Glu Lys Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser
65              70              75

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80 85 90	
ttg gat gat gcc tta aga ctt att gaa caa ccg gaa ttg gca agt aaa	339
Leu Asp Asp Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys	
95 100 105	
gta gac atg gtt tgg ata gtc gga ggc agt tct gtt tac cag gaa gcc	387
Val Asp Met Val Trp Ile Val Gly Gly Ser Val Tyr Gln Glu Ala	
110 115 120 125	
atg aat caa cca ggc cac ctt aga ctc ttt gtg aca agg atc atg cag	435
Met Asn Gln Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln	
130 135 140	
gaa ttt gaa agt gac acg ttt ttc cca gaa att gat ttg ggg aaa tat	483
Glu Phe Glu Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr	
145 150 155	
aaa ctt ctc cca gaa tac cca ggc gtc ctc tct gag gtc cag gag gaa	531
Lys Leu Leu Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu	
160 165 170	
aaa ggc atc aag tat aag ttt gaa gtc tac gag aag aaa gac	573
Lys Gly Ile Lys Tyr Lys Phe Glu Val Tyr Glu Lys Lys Asp	
175 180 185	
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Lys Tyr Phe Gln Arg Met Thr Thr Thr Ser Ser Val Glu Gly Lys Gln	
35 40 45	
Asn Leu Val Ile Met Gly Arg Lys Thr Trp Phe Ser Ile Pro Glu Lys	
50 55 60	

Asn Arg Pro Leu Lys Asp Arg Ile Asn Ile Val Leu Ser Arg Glu Leu
65 70 75 80

Lys Glu Pro Pro Arg Gly Ala His Phe Leu Ala Lys Ser Leu Asp Asp
85 90 95

Ala Leu Arg Leu Ile Glu Gln Pro Glu Leu Ala Ser Lys Val Asp Met
100 105 110

Val Trp Ile Val Gly Gly Ser Ser Val Tyr Gln Glu Ala Met Asn Gln
115 120 125

Pro Gly His Leu Arg Leu Phe Val Thr Arg Ile Met Gln Glu Phe Glu
130 135 140

Ser Asp Thr Phe Phe Pro Glu Ile Asp Leu Gly Lys Tyr Lys Leu Leu
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Pro Glu Tyr Pro Gly Val Leu Ser Glu Val Gln Glu Glu Lys Gly Ile
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 taggcacga attc 134

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 gggacgctag taaccatggg cttgctgact taggcacga attcatcaag cttatcgata 240
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28

<210> 26
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1 5 10 15		
ctg atg agc gct cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc		96
Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile		
20 25 30		
atc cag gcc gag ttc tat ctg aat cct gac caa tca ggc gag ttt atg		144
Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met		
35 40 45		
ttt gac ttt gat ggt gat gag att ttc cat gtg gat atg gca aag aag		192
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys		
50 55 60		
gag acg gtc tgg cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag		240
Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu		
65 70 75 80		
gct caa ggt gca ttg gcc aac ata gct gtg gac aaa gcc aac ttg gaa		288
Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu		
85 90 95		
atc atg aca aag cgc tcc aac tat act ccg atc acc aat gta cct cca		336
Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro		
100 105 110		
gag gta act gtg ctc acg aac agc cct gtg gaa ctg aga gag ccc aac		384
Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn		
115 120 125		

gtc ctc atc tgt ttc ata gac aag ttc acc cca cca gtg gtc aat gtc	432
Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val	
130 135 140	
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Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr	
145 150 155 160	
gtc ttc ctg ccc agg gaa gac cac ctt ttc cgc aag ttc cac tat ctc	528
Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu	
165 170 175	
ccc ttc ctg ccc tca act gag gac gtt tac gac tgc agg gtg gag cac	576
Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His	
180 185 190	
tgg ggc ttg gat gag cct ctt ctc aag cac tgg gag ttt gat gct cca	624
Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro	
195 200 205	
agc cct ctc cca aat aaa gga agt gga acc act tca ggt act acc cgt	672
Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg	
210 215 220	
ctt cta tct ggg cac acg tgt ttc acg ttg aca ggt ttg ctt ggg acg	720
Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr	
225 230 235 240	
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Leu Val Thr Met Gly Leu Leu Thr	
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<210> 27
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<400> 27

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Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met	
35 40 45	
Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys	
50 55 60	

Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
65 70 75 80

Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
85 90 95

Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
100 105 110

Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
115 120 125

Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
130 135 140

Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
145 150 155 160

Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
165 170 175

Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
180 185 190

Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
195 200 205

Ser Pro Leu Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg
210 215 220

Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr
225 230 235 240

Leu Val Thr Met Gly Leu Leu Thr
245

<210> 28
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 28
ccacttcctt tatttggtgc agattcag

28

<210> 29
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(783)

<400> 29
 atg gtg tgt ctg aag ctc cct gga ggc tcc tgc atg aca gcg ctg aca 48
 Met Val Cys Leu Lys Leu Pro Gly Gly Ser Cys Met Thr Ala Leu Thr
 1 5 10 15

gtg aca ctg atg gtg ctg agc tcc cga ctg gct ttg gct ggg gac acc 96
 Val Thr Leu Met Val Leu Ser Ser Arg Leu Ala Leu Ala Gly Asp Thr
 20 25 30

cga cca cgt ttc ttg tgg cag ctt aag ttt gaa tgt cat ttc ttc aat 144
 Arg Pro Arg Phe Leu Trp Gln Leu Lys Phe Glu Cys His Phe Phe Asn
 35 40 45

ggg acg gag cgg gtg cgg ttg ctg gaa aga tgc atc tat aac caa gag 192
 Gly Thr Glu Arg Val Arg Leu Leu Glu Arg Cys Ile Tyr Asn Gln Glu
 50 55 60

gag tcc gtg cgc ttc gac agc gac gtg ggg gag tac cgg gcg gtt gag 240
 Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Glu
 65 70 75 80

gag ctg ggg cgg cct gat gcc gag tac tgg aac agc cag aag gac ctc 288
 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85 90 95

ctg gag cag aag cgg ggc cag gtg gac aat tac tgc aga cac aac tac 336
 Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
 100 105 110

ggg gtt ggt gag agc ttc aca gtg cag cgg cga gtt gag cct aag gtg 384
 Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
 115 120 125

act gtg tat cct tca aag acc cag ccc ctg cag cac cac aac ctc ctg 432
 Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
 130 135 140

gtc tgc tct gtg agt ggt ttc tat cca ggc agc att gaa gtc agg tgg 480
 Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
 145 150 155 160

ttc cgg aac ggc cag gaa gag aag gct ggg gtg gtg tcc acg ggc ctg 528
 Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
 165 170 175

atc	cag	aat	gga	gat	tgg	acc	ttc	cag	acc	ctg	gtg	atg	ctg	gaa	ata	576
Ile	Gln	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Thr	Leu	Val	Met	Leu	Glu	Ile	
			180					185					190			

gtt	cct	cgg	agt	gga	gag	gtt	tac	acc	tgc	caa	gtg	gag	cac	cca	agt	624
Val	Pro	Arg	Ser	Gly	Glu	Val	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Ser	
		195					200					205				

gtg	acg	agc	cct	ctc	aca	gtg	gaa	tgg	aga	gca	cgg	tct	gaa	tct	gca	672
Val	Thr	Ser	Pro	Leu	Thr	Val	Glu	Trp	Arg	Ala	Arg	Ser	Glu	Ser	Ala	
	210					215					220					

cca	aat	aaa	gga	agt	gga	acc	act	tca	ggt	act	acc	cgt	ctt	cta	tct	720
Pro	Asn	Lys	Gly	Ser	Gly	Thr	Thr	Ser	Gly	Thr	Thr	Arg	Leu	Leu	Ser	
225					230					235					240	

ggg	cac	acg	tgt	ttc	acg	ttg	aca	ggt	ttg	ctt	ggg	acg	cta	gta	acc	768
Gly	His	Thr	Cys	Phe	Thr	Leu	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Val	Thr	
				245					250					255		

atg	ggc	ttg	ctg	act	tag	786
Met	Gly	Leu	Leu	Thr		
			260			

<210> 30
 <211> 261
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 30

Met	Val	Cys	Leu	Lys	Leu	Pro	Gly	Gly	Ser	Cys	Met	Thr	Ala	Leu	Thr
1				5					10					15	

Val	Thr	Leu	Met	Val	Leu	Ser	Ser	Arg	Leu	Ala	Leu	Ala	Gly	Asp	Thr
			20					25					30		

Arg	Pro	Arg	Phe	Leu	Trp	Gln	Leu	Lys	Phe	Glu	Cys	His	Phe	Phe	Asn
		35					40					45			

Gly	Thr	Glu	Arg	Val	Arg	Leu	Leu	Glu	Arg	Cys	Ile	Tyr	Asn	Gln	Glu
	50					55					60				

Glu	Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Glu
65					70					75					80

Glu	Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Leu
				85					90					95	

Leu Glu Gln Lys Arg Gly Gln Val Asp Asn Tyr Cys Arg His Asn Tyr
100 105 110

Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Glu Pro Lys Val
115 120 125

Thr Val Tyr Pro Ser Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
130 135 140

Val Cys Ser Val Ser Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
145 150 155 160

Phe Arg Asn Gly Gln Glu Glu Lys Ala Gly Val Val Ser Thr Gly Leu
165 170 175

Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Ile
180 185 190

Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
195 200 205

Val Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
210 215 220

Pro Asn Lys Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser
225 230 235 240

Gly His Thr Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr
245 250 255

Met Gly Leu Leu Thr
260

<210> 31
 <211> 189
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(186)

<400> 31
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15
 cca ttt tgg gaa gat act aca gag aac gtg gtg tgt gcc ctg ggc ctg 96
 Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
 20 25 30
 act gtg ggt ctg gtg ggc atc att att ggg acc atc ttc atc atc aag 144
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45
 gga gtg cgc aaa agc aat gca gca gaa cgc agg ggg cct ctg taa 189
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

<210> 32
 <211> 62
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 32
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15
 Pro Phe Trp Glu Asp Thr Thr Glu Asn Val Val Cys Ala Leu Gly Leu
 20 25 30
 Thr Val Gly Leu Val Gly Ile Ile Ile Gly Thr Ile Phe Ile Ile Lys
 35 40 45
 Gly Val Arg Lys Ser Asn Ala Ala Glu Arg Arg Gly Pro Leu
 50 55 60

<210> 33
 <211> 192
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(189)

<400> 33
 ttg gat cca cga tcg ttt cta ttg cgc aat cca aat gat aag tac gaa 48
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15
 cca ttt tgg gaa gat cag agc aag atg ctg agt gga gtc ggg ggc ttc 96
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
 20 25 30
 gtg ctg ggc ctg ctc ttc ctt ggg gcc ggg ctg ttc atc tac ttc agg 144
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
 35 40 45
 aat cag aaa gga cac tct gga ctt cag cca aca gga ttc ctg agc tga 192
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
 50 55 60

<210> 34
 <211> 63
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 34
 Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro Asn Asp Lys Tyr Glu
 1 5 10 15
 Pro Phe Trp Glu Asp Gln Ser Lys Met Leu Ser Gly Val Gly Gly Phe
 20 25 30
 Val Leu Gly Leu Leu Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg
 35 40 45
 Asn Gln Lys Gly His Ser Gly Leu Gln Pro Thr Gly Phe Leu Ser
 50 55 60

<210> 35
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 35
 cgatcgtgga tccaagttta gggtcgtatc tgtttcaaa 39

 <210> 36
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 36
 cgatcgagga tccaagatgg tggcagacag gacc 34

 <210> 37
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 37
 acgcgtccac catggccata agtggagtcc ct 32

 <210> 38
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 38
 ggatccaact ctgtagtctc tgggagag 28

<210> 39
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 39
 acgcgtccac catggtgtgt ctgaagctcc tg 32

<210> 40
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 40
 ggatccaact tgctctgtgc agattcaga 29

<210> 41
 <211> 292
 <212> DNA
 <213> Homo sapiens

 <400> 41
 gaattctttt ttgcgtgtgg cagttttaag ttattagttt ttaaaatcag tacttttttaa 60
 tggaacaac ttgacaaaa atttgtcaca gaattttgag acccattaaa aaagttaa 120
 gagaaacctg tgtgttcctt tggtaaacac cgagacattt aggtgaaaga catctaattc 180
 tggttttacg aatctggaaa cttcttgaaa atgtaattct tgagttaaca cttctgggtg 240
 gagaataggg ttgttttccc cccacataat tggaagggga aggaatatcg at 292

<210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 42
 tcgatggcgc gccttaatta 20

<210> 43
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 43
 agcttaatta aggcgcgcca 20

<210> 44
 <211> 1147
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 44
 gcggccgcgt cgaccaaggg ccccgagcgtg ttccccctgg ccccctgctc ccgcagcacc 60
 agcggcgggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc 120
 gtgagctgga acagcggcgc cctgaccagc ggcgctccaca ccttccccgc cgtgctgcag 180
 tccagcggcc tgtactccct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 240
 cagacctaca cctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagcgcgtg 300
 gagctgaaga cccccctggg cgacaccacc cacacctgcc cccgctgccc cgagcccaag 360
 agctgcgaca cccctcccc ctgccccgc tgccccgagc ccaagagctg cgacaccct 420
 cccccctgcc cccgctgccc cgagcccaag agctgcgaca cccctcccc ctgccccgc 480
 tgccccgccc ccgagctgct gggcggcccc agcgtgttcc tgttcccccc caagcccaag 540
 gacacctga tgatctcccg ccccccgag gtgacctgcg tgggtggtgga cgtgagccac 600
 gaggaccccc aggtgcagtt caagtggtag gtggacggcg tggaggtgca taacgccaaag 660
 accaagcccc gcgaggagca gtacaacagc accttccgcg tggtagagct gctgaccgtg 720
 ctgcaccagg actggctgaa cggcaaggag tacaagtga aggtgagcaa caaggccctg 780
 cccgccccca tcgagaagac catctccaag accaagggcc agccccgca gccccaggtg 840
 tacacctgc cccccagccg cgaggagatg accaagaacc aggtgagcct gacctgcctg 900
 gtgaagggct tctacccccag cgacatcgcc gtggagtggg agagcagcgg ccagccccgag 960
 aacaactaca acaccacccc ccccatgctg gacagcgacg gcagcttctt cctgtacagc 1020
 aagctgaccg tggacaagag ccgctggcag cagggcaaca tcttctctg cagcgtgatg 1080

catgaggccc tgcacaaccg cttcacccag aagagcctga gcctgagccc cggcaagtga 1140
tagatct 1147

<210> 45
<211> 377
<212> PRT
<213> Homo sapiens

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
 195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
 225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

<210> 46
 <211> 999
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 46
 gcggccgcgc gtcgaccaag ggccccagcg tgttccccct ggccccctgc agccgcagca 60
 ccagcgagag caccgccgcc ctgggctgcc tggatgaagga ctacttcccc gagcccgta 120
 ccgtgagctg gaacagcggc gccctgacca gcggcgtagc caccttcccc gccgtgctgc 180
 agagcagcgg cctgtactcc ctgagcagcg tggatgaccgt gccagcagc agcctgggca 240
 ccaagacctc cacctgcaac gtggaccaca agcccagcaa caccaaggta gacaagcgcg 300
 tggagagcaa gtacggcccc ccctgccccca gctgccccgc ccccgagttc ctgggcggcc 360
 ccagcgtggt cctgttcccc cccaagccca aggacaccct gatgatcagc cgcacccccg 420
 aggtgacctg cgtgggtggtg gacgtgagcc agggaggacc cgaggtagcag ttcaactggt 480
 acgtggacgg cgtggagggtg cataacgcca agaccaagcc ccgcgaggag cagttcaaca 540
 gcacctaccg cgtgggtgagc gtgctgaccg tgctgcacca ggactggctg aacggcaagg 600
 agtacaagtg caagggtgtc aacaagggcc tgcccagcag catcgagaag accatcagca 660
 aggccaaggc ccagccccgc gagccccagg tgtacaccct gccccccagc caggaggaga 720
 tgaccaagaa ccagggtgagc ctgacctgcc tggatgaagg cttctacccc agcgacatcg 780
 ccgtggagtg ggagagcaac ggccagcccc agaacaacta caagaccacc cccccctgc 840
 tggacagcga cggcagcttc ttctgtaca gccgcctgac cgtggacaag agccgctggc 900
 aggagggcaa cgtgttctcc tgctccgtga tgcatgaggc cctgcacaac cactacaccc 960
 agaagagcct gagcctgagc ctgggcaagt gatagatct 999

<210> 47
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 47

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
 100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
 195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
 225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 245 250 255

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 260 265 270

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 275 280 285

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
 290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
 325

<210> 48
 <211> 337
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 48
 gcggccgcac tgtggctgca ccattctgtct tcattcttccc gccattctgat gaggcagctta 60
 agtccggaac cgccagcgtg gtgtgcctgc tgaacaactt ctacccccgc gaggccaagg 120
 tgcagtggaa ggtggacaac gccctccaga gcggcaactc ccaggagagc gtgaccgagc 180
 aggacagcaa ggacagcacc tacagcctga gcagcaccct gaccctgagc aaggccgact 240
 acgagaagca caaggtgtac gcctgcgagg tgacccatca gggcctgagc agccccgtga 300
 ccaagagctt caaccggggc gaggctagat gagatct 337

<210> 49
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 49

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 1 5 10 15

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 20 25 30

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 35 40 45

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 50 55 60

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 65 70 75 80

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 50
 <211> 346
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 50
 gcggccgcac cgtcctaggt cagcccaagg cggcgcccag cgtgaccctg ttccccccca 60
 gcagcgagga gctgcaggcc aacaaggcca ccctgggtgtg cctgatcagc gacttctacc 120
 ccggggccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc ggcggtggaga 180
 ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac ctgagcctga 240
 cccccgagca gtggaagagc caccgcagct acagctgcca ggtcaccac gagggcagca 300
 ccgtggagaa gaccgtggcc cccaccgagt gcagctagtg agatct 346

<210> 51
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 51

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
 1 5 10 15

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
 20 25 30

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
 35 40 45

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
 50 55 60

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
 65 70 75 80

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
 85 90 95

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 100 105

<210> 52
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 52
 tctagaattc acgcgtccac catggactgg acctggag 38

<210> 53
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 53
 tctagaattc acgcgtccac catggacaca ctttgctaca c 41

<210> 54
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 54
 tctagaattc acgcgtccac catggagttt gggctgagct gg 42

<210> 55
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 55
 tctagaattc acgcgtccac catgaaacac ctgtggttct tcct 44

 <210> 56
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 56
 tctagaattc acgcgtccac catgggggtca accgccatcc t 41

 <210> 57
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 57
 tctagaattc acgcgtccac catgtctgtc tccttctca tctt 44

 <210> 58
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic

 <400> 58
 gcctgagttc cacgacaccg tcac 24

<210> 59
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
ggggaaaagg gttggggcgg atgc

24

<210> 60
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60
gaggggccct tggtcgacgc tgaggagacg gtgaccagg

39

<210> 61
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
gaggggccct tggtcgacgc tgaagagacg gtgaccattg

40

<210> 62
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62
gaggggccct tggtcgacgc tgaggagacg gtgaccgtg

39

<210> 63
 <211> 45
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